OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/975,072

DATE: 10/29/2001
TIME: 16:16:19

Input Set : **A:\269conversion.txt**
Output Set: **N:\CRF3\10292001\I975072.raw**

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   3 <110> APPLICANT: Roch, Jean-Marc
   4        Bartel, Paul L.
   5        Heichman, Karen
   7 <120> TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
   8        Diseases
  10 <130> FILE REFERENCE: Protein Interactions in ND
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C--> 12 **<140> CURRENT APPLICATION NUMBER: US/09/975,072**
C--> 13 **<141> CURRENT FILING DATE: 2001-10-12**
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  15 <150> PRIOR APPLICATION NUMBER: US 60/240,790
  16 <151> PRIOR FILING DATE: 2000-10-17
  18 <160> NUMBER OF SEQ ID NOS: 4
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  24 <212> TYPE: DNA
  25 <213> ORGANISM: Artificial Sequence
  27 <220> FEATURE:
  28 <223> OTHER INFORMATION: Description of Artificial Sequence:tail for
  29        forward primer for yeast two-hybrid system
  31 <400> SEQUENCE: 1
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  38 <213> ORGANISM: Artificial Sequence
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  55 <222> LOCATION: (217)..(1332)
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  62 taattaaaac atttttcagg gacgtagcca tccagagaca ttccattatt gttccattga 180
  64 cctttccctc atcactgagt cctttggagc tgagtt atg tca aca gct gcc tta   234
  65                                           Met Ser Thr Ala Ala Leu
  66                                             1               5
  68 att act ttg gtc aga agt ggt ggg aac cag gtg aga agg aga gtg ctg   282
  69 Ile Thr Leu Val Arg Ser Gly Gly Asn Gln Val Arg Arg Arg Val Leu
  70               10              15              20
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72 cta agc tcc cgc ctg ctg cag gac gac agg cgg gtg aca ccc acg tgc   330
73 Leu Ser Ser Arg Leu Leu Gln Asp Asp Arg Arg Val Thr Pro Thr Cys
74         25                  30                  35
76 cac agc tcc act tca gag cct agg tgt tct cgg ttt gac cca gat ggt   378
77 His Ser Ser Thr Ser Glu Pro Arg Cys Ser Arg Phe Asp Pro Asp Gly
78         40                  45                  50
80 agt ggg agt cca gct acc tgg gac aat ttt ggg atc tgg gat aac cgc   426
81 Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe Gly Ile Trp Asp Asn Arg
82 55                  60                  65                  70
84 att gat gag cca att ctg ctg cca ccc agc att aag tat ggc aag cca   474
85 Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser Ile Lys Tyr Gly Lys Pro
86                  75                  80                  85
88 att ccc aaa atc agc ttg gaa aat gtg ggg tgc gcc tca cag att ggc   522
89 Ile Pro Lys Ile Ser Leu Glu Asn Val Gly Cys Ala Ser Gln Ile Gly
90                  90                  95                  100
92 aaa cgg aaa gag aat gaa gat cgg ttt gac ttc gct cag ctg aca gat   570
93 Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp Phe Ala Gln Leu Thr Asp
94         105                 110                 115
96 gag gtc ctg tac ttt gca gtg tat gat gga cac ggt gga cct gca gca   618
97 Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly His Gly Gly Pro Ala Ala
98     120                 125                 130
100 gct gat ttc tgt cat acc cac atg gag aaa tgt att atg gat ttg ctt   666
101 Ala Asp Phe Cys His Thr His Met Glu Lys Cys Ile Met Asp Leu Leu
102 135                 140                 145                 150
104 cct aag gag aag aac ttg gaa act ctg ttg acc ttg gct ttt cta gaa   714
105 Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu Thr Leu Ala Phe Leu Glu
106                 155                 160                 165
108 ata gat aaa gcc ttt tcg agt cat gcc cgc ctg tct gct gat gca act   762
109 Ile Asp Lys Ala Phe Ser Ser His Ala Arg Leu Ser Ala Asp Ala Thr
110                 170                 175                 180
112 ctt ctg acc tct ggg act act gca aca gta gcc cta ttg cga gat ggt   810
113 Leu Leu Thr Ser Gly Thr Thr Ala Thr Val Ala Leu Leu Arg Asp Gly
114             185                 190                 195
116 att gaa ctg gtt gta gcc agt gtt ggg gac agc cgg gct att ttg tgt   858
117 Ile Glu Leu Val Val Ala Ser Val Gly Asp Ser Arg Ala Ile Leu Cys
118     200                 205                 210
120 aga aaa gga aaa ccc atg aag ctg acc att gac cat act cca gaa aga   906
121 Arg Lys Gly Lys Pro Met Lys Leu Thr Ile Asp His Thr Pro Glu Arg
122 215                 220                 225                 230
124 aaa gat gaa aaa gaa agg atc aag aaa tgt ggt ggt ttt gta gct tgg   954
125 Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys Gly Gly Phe Val Ala Trp
126                 235                 240                 245
128 aat agt ttg ggg cag cct cac gta aat ggc agg ctt gca atg aca aga   1002
129 Asn Ser Leu Gly Gln Pro His Val Asn Gly Arg Leu Ala Met Thr Arg
130             250                 255                 260
132 agt att gga gat ttg gac ctt aag acc agt ggt gtc ata gca gaa cct   1050
133 Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser Gly Val Ile Ala Glu Pro
134         265                 270                 275
136 gaa act aag agg att aag tta cat cat gct gat gac agc ttc ctg gtc   1098
```

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137 Glu Thr Lys Arg Ile Lys Leu His His Ala Asp Asp Ser Phe Leu Val
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140 ctc acc aca gat gga att aac ttc atg gtg aat agt caa gag att tgt   1146
141 Leu Thr Thr Asp Gly Ile Asn Phe Met Val Asn Ser Gln Glu Ile Cys
142 295                 300                 305                 310
144 gac ttt gtc aat cag tgc cat gat ccc aac gaa gca gcc cat gcg gtg   1194
145 Asp Phe Val Asn Gln Cys His Asp Pro Asn Glu Ala Ala His Ala Val
146                 315                 320                 325
148 act gaa cag gca ata cag tac ggt act gag gat aac agt act gca gta   1242
149 Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu Asp Asn Ser Thr Ala Val
150                 330                 335                 340
152 gta gtg cct ttt ggt gcc tgg gga aaa tat aag aac tct gaa atc aac   1290
153 Val Val Pro Phe Gly Ala Trp Gly Lys Tyr Lys Asn Ser Glu Ile Asn
154                 345                 350                 355
156 ttc tca ttc agc aga agc ttt gcc tcc agt gga cga tgg gcc           1332
157 Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser Gly Arg Trp Ala
158     360                 365                 370
160 tgattaccag ctgggactta gagtttctgt gcaacagttt ttcactgagc atgtcaagaa 1392
162 actgataaga tcaaaaaggt ctcctaactc actagatcag cgcacaagtc agtgtaaacc 1452
164 acttagatag tagttttttc ataaatgctc atcatattta tgttccgctg tacatgttca 1512
166 gtataaatat atgtgtagtg aagctactgt gagtctttaa atggaaagag caaatgagaa 1572
168 gtggtttgga tacacttgat gagagatgag agtgtcacat taataatttt taagactctt 1632
170 aggcagctat gggtttcttt tgatcatttt tgttctttat tcatttgaac acgtttttga 1692
172 agttcttcaa aactagtcag tttgaatttt gacagctatt caatatgtga tctccaagtt 1752
174 taaaaaaatt tttttccaga cttccctaat cctaaaatgc gagtttttat ttttaataac 1812
176 tgtaccaagg aataagtatg aaaacagttc tctgttacca tattttgtat tctggaccac 1872
178 ttactggtga aagcaaccat gcaaaagaaa ttaatttggc caggcacagt ggctcatgcc 1932
180 tgtaatccca aattgctggg attacagcac tgtgccctcc taggaaatta ttttttaagt 1992
182 gaaattttat ttttattttt tttaggattt tggtagagaa tgagtaggcc tactcatcaa 2052
184 tatcaaacag gacatttagt ttctttcctt agaacagaca taaatttaat ttcatggtaa 2112
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190 cgcttatata gatgacttag gcagaaataa agtcatgtct ttagaaggtg aacaagccaa 2292
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196 tcatggagtt cttccacttc caagaatgac tcatttgctg ttggattcta gtacagaatt 2472
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200 tgttttgtaa tttaccaaag tactacctga gtgtataatg actcctgcag tgagttaatg 2592
202 taattgctgc tttgaccatt gttttaaatc tgtgtactag agtaactgtg agcagaatga 2652
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206 taaaaaaaac aaaaaaaaaa aaaaaaa                                      2740
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221 Arg Val Thr Pro Thr Cys His Ser Ser Thr Ser Glu Pro Arg Cys Ser
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224 Arg Phe Asp Pro Asp Gly Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe
225     50              55                    60
227 Gly Ile Trp Asp Asn Arg Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser
228 65              70                    75                    80
230 Ile Lys Tyr Gly Lys Pro Ile Pro Lys Ile Ser Leu Glu Asn Val Gly
231             85              90                    95
233 Cys Ala Ser Gln Ile Gly Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp
234         100             105                   110
236 Phe Ala Gln Leu Thr Asp Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly
237         115             120                   125
239 His Gly Gly Pro Ala Ala Ala Asp Phe Cys His Thr His Met Glu Lys
240     130             135                   140
242 Cys Ile Met Asp Leu Leu Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu
243 145             150                   155                   160
245 Thr Leu Ala Phe Leu Glu Ile Asp Lys Ala Phe Ser Ser His Ala Arg
246             165                   170                   175
248 Leu Ser Ala Asp Ala Thr Leu Leu Thr Ser Gly Thr Thr Ala Thr Val
249         180                   185                   190
251 Ala Leu Leu Arg Asp Gly Ile Glu Leu Val Val Ala Ser Val Gly Asp
252         195                   200                   205
254 Ser Arg Ala Ile Leu Cys Arg Lys Gly Lys Pro Met Lys Leu Thr Ile
255     210             215                   220
257 Asp His Thr Pro Glu Arg Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys
258 225             230                   235                   240
260 Gly Gly Phe Val Ala Trp Asn Ser Leu Gly Gln Pro His Val Asn Gly
261             245                   250                   255
263 Arg Leu Ala Met Thr Arg Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser
264         260             265                   270
266 Gly Val Ile Ala Glu Pro Glu Thr Lys Arg Ile Lys Leu His His Ala
267         275             280                   285
269 Asp Asp Ser Phe Leu Val Leu Thr Thr Asp Gly Ile Asn Phe Met Val
270     290             295                   300
272 Asn Ser Gln Glu Ile Cys Asp Phe Val Asn Gln Cys His Asp Pro Asn
273 305             310                   315                   320
275 Glu Ala Ala His Ala Val Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu
276             325                   330                   335
278 Asp Asn Ser Thr Ala Val Val Val Pro Phe Gly Ala Trp Gly Lys Tyr
279         340             345                   350
281 Lys Asn Ser Glu Ile Asn Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser
282         355             360                   365
284 Gly Arg Trp Ala
285     370
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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date